

## SEQUENCE LISTING

&lt;110&gt; Bayer CropScience Aktiengesellschaft

&lt;120&gt; Helicokinin receptor

&lt;130&gt; Le A 36 033

&lt;160&gt; 2

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 1452

&lt;212&gt; DNA

&lt;213&gt; Heliothis virescens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1452)

&lt;223&gt;

&lt;400&gt; 1

atg gac act agt aca aca aat tca tca caa gat gac gac gcg gac tgg	48
Met Asp Thr Ser Thr Thr Asn Ser Ser Gln Asp Asp Asp Ala Asp Trp	
1 5 10 15	

cca agg aac agt tcc att gac gag tat att ata cac aat gga act aat	96
Pro Arg Asn Ser Ser Ile Asp Glu Tyr Ile Ile His Asn Gly Thr Asn	
20 25 30	

gat aca ttc gaa aca ttg tac gat gtg ccg act ggt atg ata gta ctc	144
Asp Thr Phe Glu Thr Leu Tyr Asp Val Pro Thr Gly Met Ile Val Leu	
35 40 45	

ttg tcg ttc ctg tac ggc tca ata tca gtt ctt gcg gtg gtg ggg aac	192
Leu Ser Phe Leu Tyr Gly Ser Ile Ser Val Leu Ala Val Val Gly Asn	
50 55 60	

ttt ctg gtg atg tgg gtc gtg gcc acc tcg aga aga atg cag agc gtc	240
Phe Leu Val Met Trp Val Val Ala Thr Ser Arg Arg Met Gln Ser Val	
65 70 75 80	

aca aac tgc tac ata gcc aac tta gct tta gct gac ata gtc ata gga	288
Thr Asn Cys Tyr Ile Ala Asn Leu Ala Leu Ala Asp Ile Val Ile Gly	
85 90 95	

tta ttc gct gta cca ttt caa ttt caa gcc gcg ctg cta cag cgg tgg	336
Leu Phe Ala Val Pro Phe Gln Phe Gln Ala Ala Leu Leu Gln Arg Trp	
100 105 110	

ctg cta ccg cac ttc atg tgt ccg ttc tgc ccg ttc gtg cag gcg ctc	384
Leu Leu Pro His Phe Met Cys Pro Phe Cys Pro Phe Val Gln Ala Leu	
115 120 125	

agt gtc aac gtc agc gtg ttt aca ctg aca gcc atc gca gtt gac aga	432
Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala Ile Ala Val Asp Arg	
130 135 140	

cat ccg gcg ata atc aca ccg ctc agc gcc cac act tca aag cgt att	480
His Arg Ala Ile Ile Thr Pro Leu Ser Ala His Thr Ser Lys Arg Ile	
145 150 155 160	

gcc aaa gta ata ata gtg gtt ata tgg ttt ctg gcg ctt tct tta gct	528
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Ala Lys Val Ile Ile Val Val Ile Trp Phe Leu Ala Leu Ser Leu Ala			
165	170	175	
gct ccg atg gct atg tct tgg gag gtt atc atg gaa gat gaa tta gat			576
Ala Pro Met Ala Met Ser Trp Glu Val Ile Met Glu Asp Glu Leu Asp			
180	185	190	
cca gtt gca aaa atc ttc tac aaa aag ccg ttt tgt gca ccc acc gag			624
Pro Val Ala Lys Ile Phe Tyr Lys Lys Pro Phe Cys Ala Pro Thr Glu			
195	200	205	
ttc ggc tcg cat tca ctc gcc att tat aga ctg ttg ttg tat gta ttt			672
Phe Gly Ser His Ser Leu Ala Ile Tyr Arg Leu Leu Leu Tyr Val Phe			
210	215	220	
cag tat gta atc ccg ttg tgt gtg att acg ttt gcc tac gct cat atg			720
Gln Tyr Val Ile Pro Leu Cys Val Ile Thr Phe Ala Tyr Ala His Met			
225	230	235	240
gcg atg aag ctg tgg gga gcg cgc gcc cca ggg aac gcg cag gag acg			768
Ala Met Lys Leu Trp Gly Ala Arg Ala Pro Gly Asn Ala Gln Glu Thr			
245	250	255	
agg gac gct aac cac atg cga aac aag aag gtg ata aaa atg ttg			816
Arg Asp Ala Asn His Met Arg Asn Lys Lys Val Ile Lys Met Leu			
260	265	270	
gtg ctg gtc gta gct ctg ttt gcg tta tgc tgg ctg ccg cta cag agc			864
Val Leu Val Val Ala Leu Phe Ala Leu Cys Trp Leu Pro Leu Gln Ser			
275	280	285	
tac tta tta cta caa tca ttt ttt cca tca att aac gag tac aag tac			912
Tyr Leu Leu Leu Gln Ser Phe Phe Pro Ser Ile Asn Glu Tyr Lys Tyr			
290	295	300	
atc aac gtg ctt ttc ttt tgc ttc gac tgg cta gca atg agc aac tct			960
Ile Asn Val Leu Phe Phe Cys Phe Asp Trp Leu Ala Met Ser Asn Ser			
305	310	315	320
tgc tat aac cca ttc atc tat gcc atc tac aac gaa aaa ttc aag aag			1008
Cys Tyr Asn Pro Phe Ile Tyr Ala Ile Tyr Asn Glu Lys Phe Lys Lys			
325	330	335	
gaa ttc aaa caa cga ttc act ttc ggg aaa aag cca agc aga ttc gtt			1056
Glu Phe Lys Gln Arg Phe Thr Phe Gly Lys Lys Pro Ser Arg Phe Val			
340	345	350	
aac gat agc tac gag gac ggc cag tca tac cga aca aga att tta tcg			1104
Asn Asp Ser Tyr Glu Asp Gly Gln Ser Tyr Arg Thr Arg Ile Leu Ser			
355	360	365	
ttc cga tca acc aac gac aga agt ggc tat tca tcc aga aag tct ttg			1152
Phe Arg Ser Thr Asn Asp Arg Ser Gly Tyr Ser Ser Arg Lys Ser Leu			
370	375	380	
aac ata ccg ccg ggg gac act tta aaa gtt cct tct aga aat tca tgt			1200
Asn Ile Pro Pro Gly Asp Thr Leu Lys Val Pro Ser Arg Asn Ser Cys			
385	390	395	400
cat tgc atg gcg aat cag agc aga gaa aat gga ttt aac ttc atg aaa			1248
His Cys Met Ala Asn Gln Ser Arg Glu Asn Gly Phe Asn Phe Met Lys			
405	410	415	
act gaa gac atg gaa ggg cac gga aat agc agg cgg tat ctg aat ata			1296
Thr Glu Asp Met Glu Gly His Gly Asn Ser Arg Arg Tyr Leu Asn Ile			

420	425	430	
aga atg agt aat cca gat att ggt aaa aga aga tta gct aag aag tta Arg Met Ser Asn Pro Asp Ile Gly Lys Arg Arg Leu Ala Lys Lys Leu	440	445	1344
435			
tcg aat aga gac gac atg cct ata ggt gat gag aga gtc agt gaa ctg Ser Asn Arg Asp Asp Met Pro Ile Gly Asp Glu Arg Val Ser Glu Leu	455	460	1392
450			
tac ata ttc cca aac agt aac att gta gaa ttt aca gac ata tca tac Tyr Ile Phe Pro Asn Ser Asn Ile Val Glu Phe Thr Asp Ile Ser Tyr	470	475	1440
465			
475			
gat gac aaa gtg Asp Asp Lys Val			1452

<210> 2  
<211> 484  
<212> PRT  
<213> Heliothis virescens

<400> 2

Met Asp Thr Ser Thr Thr Asn Ser Ser Gln Asp Asp Asp Ala Asp Trp  
1 5 10 15

Pro Arg Asn Ser Ser Ile Asp Glu Tyr Ile Ile His Asn Gly Thr Asn  
20 25 30

Asp Thr Phe Glu Thr Leu Tyr Asp Val Pro Thr Gly Met Ile Val Leu  
35 40 45

Leu Ser Phe Leu Tyr Gly Ser Ile Ser Val Leu Ala Val Val Gly Asn  
50 55 60

Phe Leu Val Met Trp Val Val Ala Thr Ser Arg Arg Met Gln Ser Val  
65 70 75 80

Thr Asn Cys Tyr Ile Ala Asn Leu Ala Leu Ala Asp Ile Val Ile Gly  
85 90 95

Leu Phe Ala Val Pro Phe Gln Phe Gln Ala Ala Leu Leu Gln Arg Trp  
100 105 110

Leu Leu Pro His Phe Met Cys Pro Phe Cys Pro Phe Val Gln Ala Leu  
115 120 125

Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala Ile Ala Val Asp Arg  
130 135 140

His Arg Ala Ile Ile Thr Pro Leu Ser Ala His Thr Ser Lys Arg Ile  
145 150 155 160

Ala Lys Val Ile Ile Val Val Ile Trp Phe Leu Ala Leu Ser Leu Ala  
165 170 175

Ala Pro Met Ala Met Ser Trp Glu Val Ile Met Glu Asp Glu Leu Asp  
180 185 190

Pro Val Ala Lys Ile Phe Tyr Lys Lys Pro Phe Cys Ala Pro Thr Glu  
195 200 205

Phe Gly Ser His Ser Leu Ala Ile Tyr Arg Leu Leu Leu Tyr Val Phe  
210 215 220

Gln Tyr Val Ile Pro Leu Cys Val Ile Thr Phe Ala Tyr Ala His Met  
225 230 235 240

Ala Met Lys Leu Trp Gly Ala Arg Ala Pro Gly Asn Ala Gln Glu Thr  
245 250 255

Arg Asp Ala Asn His Met Arg Asn Lys Lys Lys Val Ile Lys Met Leu  
260 265 270

Val Leu Val Val Ala Leu Phe Ala Leu Cys Trp Leu Pro Leu Gln Ser  
275 280 285

Tyr Leu Leu Leu Gln Ser Phe Phe Pro Ser Ile Asn Glu Tyr Lys Tyr  
290 295 300

Ile Asn Val Leu Phe Phe Cys Phe Asp Trp Leu Ala Met Ser Asn Ser  
305 310 315 320

Cys Tyr Asn Pro Phe Ile Tyr Ala Ile Tyr Asn Glu Lys Phe Lys Lys  
325 330 335

Glu Phe Lys Gln Arg Phe Thr Phe Gly Lys Lys Pro Ser Arg Phe Val  
340 345 350

Asn Asp Ser Tyr Glu Asp Gly Gln Ser Tyr Arg Thr Arg Ile Leu Ser  
355 360 365

Phe Arg Ser Thr Asn Asp Arg Ser Gly Tyr Ser Ser Arg Lys Ser Leu  
370 375 380

Asn Ile Pro Pro Gly Asp Thr Leu Lys Val Pro Ser Arg Asn Ser Cys  
385 390 395 400

His Cys Met Ala Asn Gln Ser Arg Glu Asn Gly Phe Asn Phe Met Lys  
405 410 415

Thr Glu Asp Met Glu Gly His Gly Asn Ser Arg Arg Tyr Leu Asn Ile  
420 425 430

Arg Met Ser Asn Pro Asp Ile Gly Lys Arg Arg Leu Ala Lys Lys Leu  
435 440 445

Ser Asn Arg Asp Asp Met Pro Ile Gly Asp Glu Arg Val Ser Glu Leu  
450 455 460

Tyr Ile Phe Pro Asn Ser Asn Ile Val Glu Phe Thr Asp Ile Ser Tyr  
465 470 475 480

Asp Asp Lys Val